



## A new species of *Cyrtodactylus* (Squamata: Gekkonidae) from Phu Yen Province, Vietnam

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### Abstract

We describe a new species of the genus *Cyrtodactylus* based on six adult specimens from Lac Dao forests, Phu Yen Province, southern Vietnam. *Cyrtodactylus tayhoaensis* **sp. nov.** is distinguished from the remaining Indochinese bent-toed geckos by a combination of the following characters: medium size (SVL up to 94.2 mm); nasal scales 5–6; internasal single or double; ciliaria 29–34; dorsal tubercles in 20–22 irregular transverse rows; ventral scale in 37–41 longitudinal rows at midbody; ventrolateral folds present without interspersed tubercles; precloacal pores absent in females, precloacal pores 4 or 5 in males; 10 or 11 enlarged femoral scales on each thigh; femoral pores 3–7 in males, absent in females; postcloacal tubercles 3 or 4; lamellae under toe IV 22–24; dorsal pattern consisting of unclear transverse bands formed by irregularly shaped dark-brown blotches, a discontinuous neckband with V-shape or triangle shape in the middle, dorsal head surface with dark-brown blotches; subcaudal scales transversely enlarged. In the phylogenetic analyses, the new species is recovered as a sister taxon to *C. kingsadai* with approximately 4% genetic divergence between the two species based on a fragment of the COI gene. This is the second species of *Cyrtodactylus* known from Phu Yen Province located in southern Vietnam.

**Key words:** *Cyrtodactylus tayhoaensis* **sp. nov.**, molecular phylogeny, taxonomy, Phu Yen Province

### Introduction

The *Cyrtodactylus irregularis* species group currently contains 24 species (except *C. badenensis*) known from southern Indochina, in particular southern Vietnam (Nazarov *et al.* 2012; Pauwels *et al.* 2018; Do *et al.* 2021; Grismer *et al.* 2021a,b; Ngo *et al.* 2022; Uetz *et al.* 2022). In the last five years, eight new species in this group have been described, namely *C. chungii* Ostrowski, Do, Le, Ngo, Pham, Nguyen, Nguyen & Ziegler; *C. culaochamensis* Ngo, Grismer, Pham & Wood; *C. gialaiensis* Luu, Tran, Nguyen, Le & Ziegler; *C. orlovi* Do, Phung, Ngo, Le, Ziegler, Pham & Nguyen; *C. phnomchiensis* Neang, Henson & Stuart; *C. phumyensis* Ostrowski, Le, Ngo, Pham, Phung, Nguyen & Ziegler; *C. raglai* Nguyen, Duong, Grismer & Poyarkov; and *C. sangi* Pauwels, Nazarov, Bobrov & Poyarkov (Do *et al.* 2021; Luu *et al.* 2017; Neang *et al.* 2020; Ngo *et al.* 2020; Nguyen *et al.* 2021; Ostrowski *et al.* 2020, 2021; Pauwels *et al.* 2018).

Recent field research in Vietnam's Phu Yen Province has led to the discovery of a so far unknown *Cyrtodactylus* population. Phu Yen Province is located in the southern Vietnam and harbors 116.819 ha of evergreen forest (Statistical Office of Phu Yen Province 2016). However, the biodiversity of this province is poorly studied, in particular the herpetofauna. Five new species were recently described from Phu Yen Province, namely *Cyrtodactylus kingsadai* Ziegler, Phung, Le & Nguyen, *Leptolalax macrops* Duong, Do, Ngo, Nguyen, & Poyarkov, *Acanthosaura murphyi* Nguyen, Do, Hoang, Nguyen, McCormack, Nguyen, Orlov, Nguyen & Nguyen, *Limnonectes phuyenensis* Pham, Do, Le, Ngo, Nguyen, Ziegler & Nguyen, and *Gekko phuyenensis* Nguyen, Nguyen, Orlov, Murphy & Nguyen (Ziegler *et al.* 2013; Duong *et al.* 2018; Nguyen *et al.* 2018; Pham *et al.* 2020; Nguyen *et al.* 2021).

During field research in Lac Dao Village, Tay Hoa District, a *Cyrtodactylus* population was found, that differs from other species of *Cyrtodactylus* in morphological characteristics and genetic divergence. It is therefore described as a new species in the following.

## Material and methods

**Sampling.** Field surveys were conducted in Lac Dao Forest, Son Thanh Tay Commune, Tay Hoa District, Phu Yen Province, Vietnam in September 2015 and September 2019 (Fig. 1). Specimens were anaesthetized and euthanized in a closed vessel with a piece of cotton wool containing ethyl acetate (Simmons 2002), fixed in 85% ethanol and subsequently stored in 70% ethanol. Specimens were subsequently deposited in the collections of the Phu Yen University (PYU), Phu Yen Province and the Institute of Ecology and Biological Resources (IEBR), Hanoi, Vietnam.

**Molecular data and phylogenetic analyses.** As the new population possesses morphological characters representing the *Cyrtodactylus irregularis* complex, we incorporated all taxa of the group (*sensu* Grismer *et al.* 2021) in the analyses. Four species, *C. condorensis* Smith, *C. grismeri* Ngo, *C. spelaeus* Nazarov, Poyarkov, Orlov, Nguyen, Milto, Martynov, Konstantinov & Chulisov, and *C. wayakonei* Nguyen, Kingsada, Rösler, Auer & Ziegler, were used as outgroups based on the results of Grismer *et al.* (2021).

DNA was extracted using DNeasy Blood and Tissue kit (Qiagen, Germany) following the manufacturer's instruction. Extracted DNA was amplified by PCR mastermix (Qiagen, Germany) with 21 µl volume (10 µl of mastermix, 5 µl of water, 2 µl of each primer at 10 pmol/ml and 2 µl of DNA). PCR condition was: 95°C for 15 minutes to active the taq; with 40 cycles at 95°C for 30 seconds, 45°C for 45 seconds, 72°C for 60 seconds; and the final extension at 72°C for 6 minutes. A fragment of the mitochondrial gene, cytochrome c oxidase subunit 1 (COI), was amplified using the primer pair VF1-d (5'-TTCTCAACCAACCACAARGAYATYGG-3') and VR1-d (5'-TAGACTTCTGGGTGGCCRAARAAYCA-3') (Ivanova *et al.* 2006). PCR products were visualized using electrophoresis through a 2% low melting-point agarose gel stained with ethidium bromide. Successful amplifications were purified to eliminate PCR components using GeneJET™ PCR Purification kit (ThermoFisher Scientific, Lithuania). Purified PCR products were sent to FirstBase (Malaysia) for sequencing in both directions.

After sequences were aligned by Clustal X v2 (Thompson *et al.* 1997), data were analyzed using maximum parsimony (MP) implemented in PAUP\*4.0b10 (Swofford 2001), maximum likelihood as implemented in IQ-TREE (Nguyen *et al.* 2015) and Bayesian inference (BI) as implemented in MrBayes v3.2 (Ronquist *et al.* 2012). For MP analysis, heuristic analysis was conducted with 100 random taxon addition replicates using tree-bisection and reconnection (TBR) branch swapping algorithm, with no upper limit set for the maximum number of trees saved. Bootstrap support (BP) was calculated using 1000 pseudo-replicates and 100 random taxon addition replicates. All characters were equally weighted and unordered. For the maximum likelihood (ML) analysis, we used IQ-TREE v.1.6.7.1 (Nguyen *et al.* 2015) with a single model and 10,000 ultrafast bootstrap replications (UFB). The optimal model for nucleotide evolution was determined using jModelTest v2.1.4 (Darriba *et al.* 2012).

For Bayesian analyses, we used the optimal model determined by jModeltest with parameters estimated by MrBayes 3.2.7. Two independent analyses with four Markov chains (one cold and three heated) were run simultaneously for 10 million generations with a random starting tree and sampled every 1000 generations. Log-likelihood scores of sample points were plotted against generation time to determine stationarity of Markov chains. Trees generated before log-likelihood scores reached stationarity were discarded from the final analyses using the burn-in function. The posterior probability values (PP) for all nodes in the final majority rule consensus tree were provided. We regard BP ≥ 70% and UFB and PP of ≥ 95% as strong support and values of <70% and < 95%, respectively, as weak support (Hillis & Bull 1993; Minh *et al.* 2013; Ronquist *et al.* 2012).



FIGURE 1. Type locality of *Cyrtodactylus tayhoaensis* sp. nov. in Phu Yen Province (purple circle), Vietnam.



The optimal model for nucleotide evolution was set to TIM2+I+G for ML analysis and GTR+I+G for Bayesian analysis as selected by jModelTest. For Bayesian analysis, the cutoff point for the burn-in function was set to 56 as  $-\ln L$  scores reached stationarity after 56,000 generations. Uncorrected pairwise divergences were calculated in PAUP\*4.0b10.

**Morphological characters.** Measurements were taken with a digital calliper to the nearest 0.1 mm. Morphological characters followed Nguyen *et al.* (2017). Abbreviations are as follows: snout-vent length (SVL), from tip of snout to vent; tail length (TaL), from vent to tip of tail (\* regenerated); head length (HL), from tip of snout to retroarticular process of jaw; head width (HW), maximum width of head; head height (HH), from occiput to underside of jaws; orbital diameter (OD), greatest diameter of orbit; snout to eye distance (SE), from tip of snout to anterior-most point of eye; eye to ear distance (EE), from anterior edge of ear opening to posterior corner of eye; nares to eye distance (NE), from anterior-most point of eye to posterior-most point of nostril; ear length (ED), longest dimension of ear; forearm length (ForeaL), from base of palm to tip of elbow; crus length (CrusL), from base of heel to knee; axilla-groin distance (AG), from axilla to groin measured from posterior edge of forelimb insertion to anterior edge of hindlimb insertion; body width (BW), the widest distance of body; internarial distance (IND), distance between nares; Interorbital distance (IOD), shortest distance between left and right supraciliary scale rows; maximum rostral width (RW); maximum rostral height (RH); maximum mental width (MW); maximum mental length (MH).

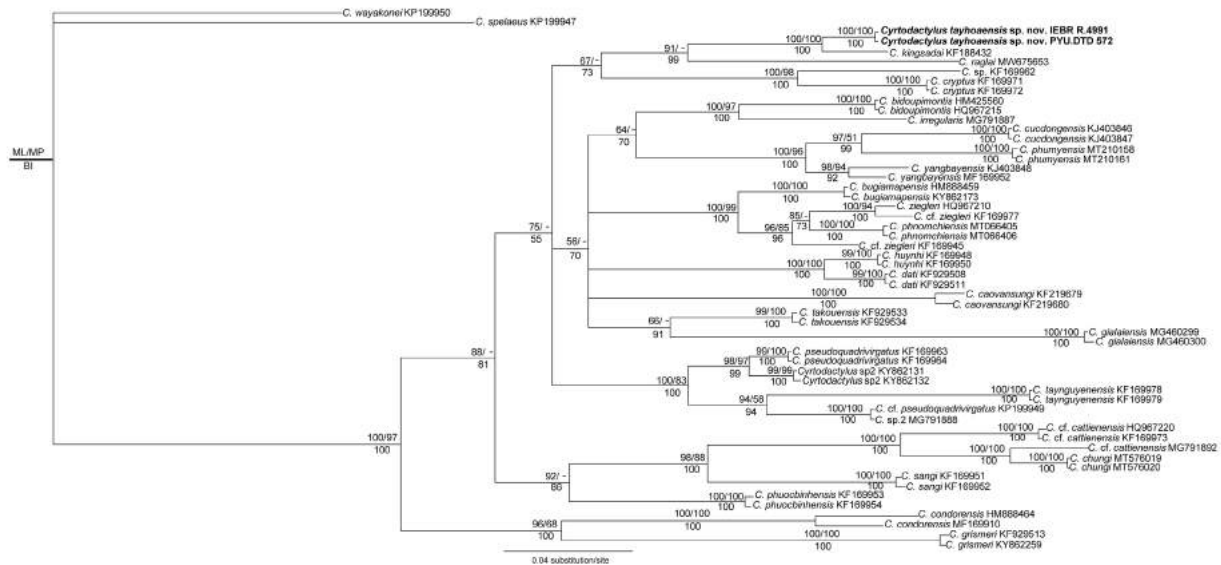
Scale counts were taken as follows: supralabials (SL), counted from the first labial scale to corner of mouth; infralabials (IL), counted from the first labial scale to corner of mouth; nasal scales surrounding nare (N); postrostrals or internasals (IN); ciliaria (CIL), scales on eyelid fringe; postmentals (PM); granular scales surrounding dorsal tubercles (GST); ventral scales in longitudinal rows at midbody (V); number of scales along the midbody from mental to anterior edge of cloaca (SLB); enlarged femoral scales (EFS), number of enlarged femoral scale beneath each thigh; femoral pores (FP); precloacal pores (PP); postcloacal tubercles (PAT); the number of dorsal longitudinal rows of tubercles at midbody between the lateral folds (TubR), number of subdigital lamellae on all fingers (NSFI, NSFII, NSFIII, NSFIV, NSFIV); number of subdigital lamellae on all toes (NSTI, NSTII, NSTIII, NSTIV, NSTV). Bilateral scale counts were given as left/right.

**Multiple Factor analysis (MFA).** We further applied a multiple factor analysis using morphometric and meristic characters in MFA were SVL, HL, HW, HH, OD, SE, SL, IL, N, V, SLB, FP, PP, DTR, EFS, NSFV and NSTIV. Other morphological characters were not used due to the limitation of available morphometric and meristic data or incomplete sampling (regenerated tail). All statistical analyses were performed using R Core Team (2018). The MFA were clustered into different groups comprising three quantitative groups - "SVL, "Head (including HL, HW, HH), "Eye and XX qualitative groups—"Species, "SL.IL (consist of SL and IL), "Nasal, "V (including V and SLB), "FP, "PP, "DTR, "EFS, "LIV (consist of NSFIV and NSTIV). To remove the effects of allometry, morphometric data were also normalized to adjust raw data of morphometrics through the `allom()` function in R package *GroupStruct* (available at <http://github.com/chankinonn/GroupStruct>). Accordingly, the allometric formula is  $X_{adj} = \log_{10}(X) - \beta[\log_{10}(SVL) - \log_{10}(SVL_{mean})]$ , where  $X_{adj}$  = adjusted value;  $X$  = measured value;  $\beta$  = unstandardized regression coefficient for each population and  $SVL_{mean}$  = overall average SVL of two populations (Thorpe 1975, 1983; Turan 1999; Leonart *et al.* 2000; Chan *et al.* 2021, Grismer *et al.* 2022). The ordination test was performed using the package *Factoextra* (Kassambara and Mundt 2017) and *FactoMinerR* (Le *et al.* 2008) in the software R. The approach was applied to identify active groups and to explain phenotypic variance by estimating the first two Dim values—eigenvalue proportions. Similar coded colors in the MFA scatter plot, surrounded with convex hulls, were presented to visualize the phenotypic spaces of *Cyrtodactylus tayhoensis* **sp. nov.** and *C. kingsadai*. Their spaces were shown within a spatial coordinate of dimension axes (Dim1 and Dim2). To evaluate the overlap, the Dim1 and Dim2 values of each *Cyrtodactylus* individual were extracted to identify the difference between the two species using the T-test. For all of the tests, we applied a significance level of  $p < 0.05$ .

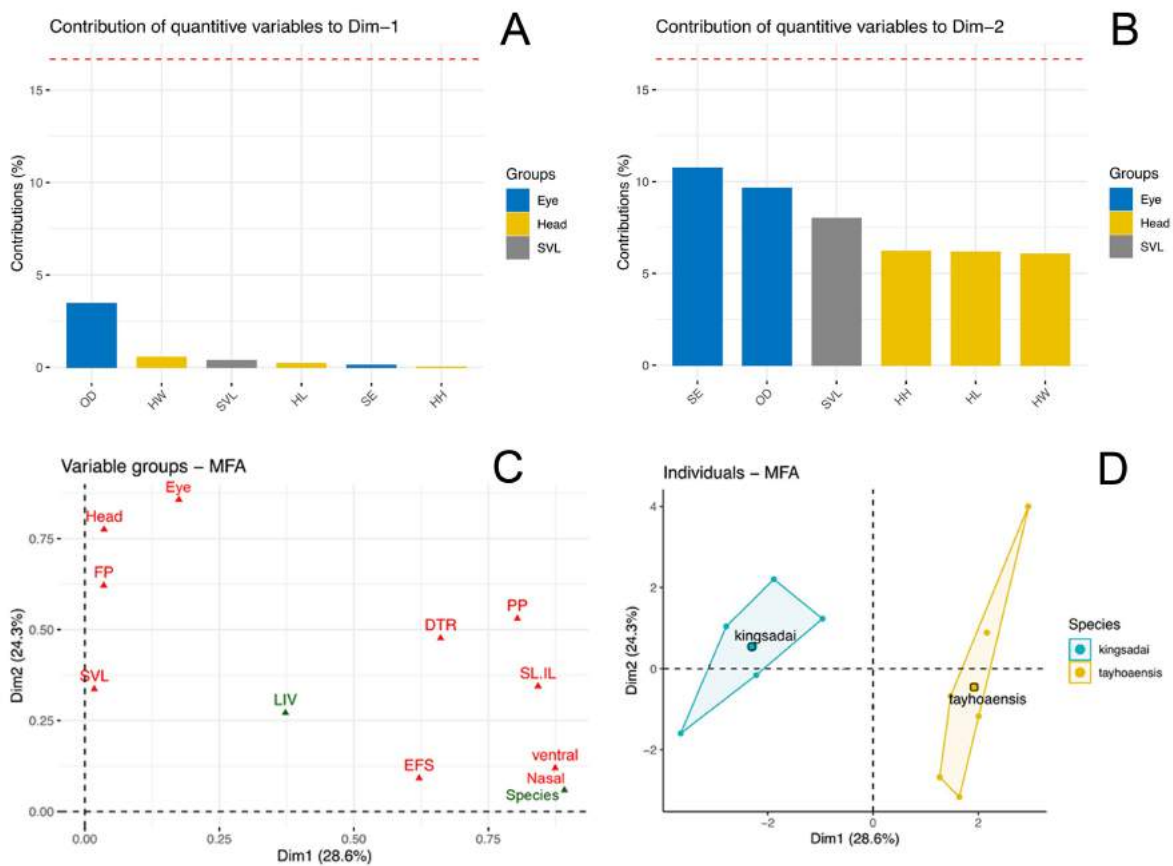
## Results

**Phylogenetic analyses.** The final matrix contained 652 aligned characters with 250 parsimony informative. MP analysis of the dataset recovered five most parsimonious trees with 1547 steps (Consistency index = 0.3; Retention index = 0.65). The topology recovered by the BI analysis was similar to that reported in Ngo *et al.* (2022). The new population from Phu Yen Province was well corroborated as a sister taxon to *C. kingsadai* also from the same province with perfect support values from all analyses (Fig. 2). The two taxa were diverged by approximately 4%

in pairwise genetic distance based on a fragment of COI (Supplementary data). They in turn were shown to be most closely related to *C. raglai* from Khanh Hoa Province with strong support found only in the BI analysis (UFB = 91%, BP <50%, PP = 99%). Based on the molecular evidence and the morphological data presented below, we hypothesize that the new population from Phu Yen Province is a new species and describe it below.



**FIGURE 2.** Phylogram based on the Bayesian analysis. Number above and below branches are ML/MP bootstrap and ultrafast bootstrap values and Bayesian posterior probabilities ( $\geq 50\%$ ), respectively.



**FIGURE 3.** (A) The first four important variables of the first axes (Dim1) in the Multiple factor analysis (MFA); (B) The first four important variables of the second axes (Dim2) in the MFA; (C) Scatterplot of all variable groups for Dim1 and Dim2 axes in the MFA, green triangles as inactive groups, red triangles as active groups or variables; (D) A MFA of *Cyrtodactylus tayhoensis* sp. nov. and *C. kingsadai*.

**Morphological analysis.** Morphologically, the new form from Tay Hoa District, Phu Yen Province is closely similar to *C. kingsadai* from Dai Lanh Cape, Tuy Hoa District, Phu Yen Province, however, they plotted separately from each other in MFA and there was a significant difference between two species ( $p < 0.05$ ). The MFA also identified the data set of SVL, Head, Eye, SL, V, EFS, FP, PP, DTR, SL as active groups (Fig. 3). Morphometrics and meristics that contributed the most to the first multi-factorial dimension were OD, HW, SVL, HL, SE, HH (Fig. 3), while SE, OD, SVL, HH, HL, HW were the most important in the second multi-factorial dimension (Fig. 3).

***Cyrtodactylus tayhoaensis* sp. nov.**

(Figs. 4–6)

**Holotype.** IEBR R.4991, adult male, collected by Dang Trong Do on 14 September 2019, in a rocky stream, near Lac Dao Village (12°53'50.0" N, 109°1'28.0" E, elevation 130 m a.s.l), Son Thanh Tay Commune, Tay Hoa District, Phu Yen Province, southern Vietnam.

**Paratypes.** IEBR R.5078, R.5079, adult females and IEBR R.4992, adult male, the same collection data as the holotype. PYU.DTD 572, adult female; PYU.DTD 573 adult male, collected by Do Trong Dang on 4 September 2015, in a rocky stream, near Lac Dao Village (12°53'13.0 N, 109°1'17.3 E, elevation 230 m a.s.l), Son Thanh Tay Commune, Tay Hoa District, Phu Yen Province, southern Vietnam.

**Diagnosis.** The new species can be distinguished from other members of the genus *Cyrtodactylus* by a combination of the following characters: medium size (SVL up to 94.2 mm); nasal scales 5–6; internasal single or double; ciliaria 29–34; dorsal tubercles in 20–22 irregular transverse rows; ventral scale rows in 37–41 longitudinal rows at midbody; ventrolateral folds present without interspersed tubercles; precloacal pores absent in females, precloacal pores 4 or 5 in males; 10 or 11 enlarged femoral scales on each thigh; femoral pores 3–7 in males, absent in females; postcloacal tubercles 3 or 4; lamellae under toe IV 22–24; dorsal pattern consisting of unclear transverse bands formed by irregularly shaped dark-brown blotches, a discontinuous neckband with V-shape or triangle shape in the middle, dorsal head surface with dark-brown blotches; subcaudal scales transversely enlarged.

**Description of holotype.** Adult male, snout-vent length (SVL) 85.5 mm; body elongate (AG/SVL 0.44); head distinct from neck, elongate, depressed (HL/SVL 0.30, HW/HL 0.66, HH/HL 0.39); eye large (OD/HL 0.27), pupils vertical; upper eyelid fringe with spinous scales; ear opening below the postocular stripes, obliquely directed and oval, small in size (ED/HL 0.08); nares oval, surrounded by supranasal, rostral, first supralabial and three postnasals; supranasals separated from each other by two nasorostrals and two pentagonal internasals; loreal region and frontal concave; snout long (SE/HL 0.44), round anteriorly, longer than diameter of orbit (OD/SE 0.61); snout scales small, round, granular, larger than those in frontal and parietal regions; rostral rectangular, wider than high (RH/RW 0.61) with a medial suture, bordered by first supralabial, nostril, internasals and supranasal on each side; mental triangular, wider than high (MH/MW 0.58); postmentals two, enlarged, in contact posteriorly, bordered by mental anteriorly, first infralabial laterally, and an enlarged chin scale posteriorly; supralabials 10/11; infralabials 9/9.

Dorsal scales granular; dorsal tubercles round, keeled, conical, four or five times larger than the size of adjoining scales, each surrounded by 9 or 10 granular scales, tubercles forming 22 irregular longitudinal rows at midbody; ventral scales smooth, medial scales 2–3 times larger than dorsal granules, round, subimbricate, largest posteriorly, in 38 longitudinal rows at midbody; lateral folds present, without interspersed tubercles; gular region with homogeneous smooth scales; ventral scales between mental and cloacal slit 143; precloacal groove absent; three rows of enlarged scales present in posterior region of pore-bearing scales; five precloacal pores arranged in a chevron; 11 enlarged femoral scales beneath thigh continuous with enlarged precloacal scales but not continuous with precloacal pores; femoral pores bearing scales enlarged, 7 in total (4 in right thigh, 3 in left thigh), separated from pore-bearing precloacal scales by poreless femoral scales.

Fore and hind limbs moderately slender (ForeL/SVL 0.17, CrusL/SVL 0.20); dorsal surface of forelimbs covered by few slightly developed tubercles; dorsal surface of hind limbs covered by slightly developed tubercles; fingers and toes lacking distinct webbing; subdigital lamellae: finger I 15, finger II 18, finger III 18, finger IV 20, finger V 18, toe I 14, toe II 18, toe III 21, toe IV 22, toe V 21.

Tail regenerated, 91.5 mm in length; longer than snout-vent length (TaL/SVL: 1.07); postcloacal tubercles 4/3; subcaudals distinctly enlarged, smooth.





**FIGURE 4.** The male holotype of *Cyrtodactylus tayhoaensis* **sp. nov.** (IEBR R.4991) in life. Photo: D.T. Do.



**FIGURE 5.** Cloacal region of the holotype of *Cyrtodactylus tayhoaensis* **sp. nov.** (IEBR R.4991) in life. Photo: D.T. Do.

**Coloration in life.** Ground color light brownish-yellow; dorsal head surface with dark-brown blotches; labials brown with yellow cream sutures; skin above the eyes yellowish blue; eyelids with light yellow color; iris yellow grey with black marking; pupil vertical, elliptical, black; a dark band crosses from the posterior of the eye to the upper border of the ear to the posterior of the nuchal area, where it runs into the V-shape with the same color on the posterior nape on each side, forming a discontinuous neckband; tubercles on head, limbs, dorsum and tail light to dark-brown; dorsal pattern consisting of six unclear transverse dark-brown bands, formed by irregular dark-brown blotches; dorsal surface of fore and hind limbs with dark-brown blotches and bars; regenerated part of tail brownish cream with dark-brown marking; chin, throat, chest, belly, lower limbs and ventral surface of tail cream.





**FIGURE 6.** A) Type series of *Cyrtodactylus tayhoensis* **sp. nov.** in preservative, B) The female paratype (IEBR R.5078) in life. Photos: D.T. Do.



**Coloration in preservative:** The overall color scheme slightly fades in 70% alcohol; yellow color disappeared in preservation; the bright yellow of the eyelids is no longer visible while main characteristics are still clearly discernible; dorsal ground color of head, neck, body, limbs and tail greyish brown; the color of chin, throat, chest, belly and lower limbs did not change noticeably in preservation.

**Sexual dimorphism and variation.** The females differ from male specimens in the absence of precloacal pores, femoral pores and hemipenial swellings at the tail base. For other morphological characters see Table 1 and Fig. 6A.

**Distribution.** *Cyrtodactylus tayhoaensis* **sp. nov.** is currently known only from the type locality in Tay Hoa District, Phu Yen Province, Vietnam (Fig. 1).

**Etymology.** Specific epithet *tayhoaensis* is a toponym in reference to the type locality of the species. For the common names we suggest Tay Hoa Bent-toed Gecko (English) and Thạch sùng ngón tây hòa (Vietnamese).

**Natural history.** The geckos were found between 19:00 and 21:00, on granite in water in rocky streams, about 0.5–1.5 m above the ground, at elevations between 130 and 230 m a.s.l. The surrounding habitat was disturbed evergreen forest of medium or small hardwood and shrub (Fig. 7). The humidity was approximately 70–80% and the air temperature ranged from 25 to 30°C.



**FIGURE 7.** Habitat of *Cyrtodactylus tayhoaensis* **sp. nov.** in Son Thanh Tay Commune, Tay Hoa District, Phu Yen Province, southern Vietnam. Photo: D.T. Do.

**Comparisons.** We compared the new species with its 24 congeners from the *Cyrtodactylus irregularis* complex based on examination of specimens and data obtained from the literature (Smith 1921a; Heidrich *et al.* 2007; Orlov *et al.* 2007; Nazarov *et al.* 2008; Ngo & Bauer 2008; Rösler *et al.* 2008; Geissler *et al.* 2009; Ngo & Chan 2010; Nazarov *et al.* 2012; Ngo 2013; Nguyen *et al.* 2013; Ziegler *et al.* 2013; Schneider *et al.* 2014; Luu *et al.* 2017; Pauwels *et al.* 2018; Ngo *et al.* 2020; Neang *et al.* 2020; Ostrowski *et al.* 2020; Ostrowski *et al.* 2021; Nguyen *et al.* 2021; Do *et al.* 2021) (see Table 2). The new species can be distinguished from all other *Cyrtodactylus* species from Vietnam by morphological characteristics (see Table 3).

Among the species of the *Cyrtodactylus irregularis* group, *Cyrtodactylus tayhoaensis* **sp. nov.** differs from its sister taxon in the phylogenetic analysis, *C. kingsadai*, by having more nasal scales surrounding nare (5–6 *versus* 4 in *C. kingsadai*), fewer scales along the midbody from mental to anterior edge of cloaca (140–157 *versus* 165–167 in *C. kingsadai*), fewer precloacal pores in males (4–5 *versus* 7–9 in *C. kingsadai*), the absence of precloacal pores in females (*versus* 4–8 in *C. kingsadai*), dark brown transversal bands of the dorsum larger than light brown interspaces (*versus* dark transversal bands as wide as light interspaces in *C. kingsadai*), and the presence of an

**TABLE 1.** Measurements (in mm) and morphological characters of the type series of *Cyrtodactylus tayhoensis* sp. nov.

(\* = regenerated or broken tail); bilateral meristic characters are given as (left/right).

Characters	IEBR R.4991		IEBR R.4992		PYU.DTD 573		IEBR R.5078		IEBR R.5079		PYU.DTD 572		Min-Max
	(Holotype)	(Paratype)	(Paratype)	(Paratype)	(Paratype)	(Paratype)	(Paratype)	(Paratype)	(Paratype)	(Paratype)	(Paratype)	(Paratype)	
Sex	M	M	M	M	F	F	F	F	F	F	F	F	
SVL	85.5	94.2	87.7	89.7	83.1	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9–94.2
TaL	91.5*	79.6*	86.1*	104.3	77.3*	101.8	101.8	101.8	101.8	101.8	101.8	101.8	max 104.3
HL	25.3	26.9	24.3	25.8	24.2	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6–26.9
HW	16.7	17.5	16.4	16.8	15.9	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7–17.5
HH	9.9	10.8	10.1	9.9	9.5	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.5–10.8
OD	6.8	7.1	6.4	6.4	6.2	6	6	6	6	6	6	6	6–7.1
SE	11.1	11.8	10.9	10.8	10.5	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2–11.8
EE	6.4	6.9	6.5	6.6	6.1	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.1–6.9
NE	8.2	8.8	8	8.3	8	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8–8.8
ED	2	2.1	2.2	1.7	2.1	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.7–2.2
ForeaL	14.8	14.3	13.3	14.6	13.5	13	13	13	13	13	13	13	13–14.8
CrusL	17.3	18.1	16.3	17.1	16.6	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8–18.1
AG	37.8	42.6	38.9	39.2	34.4	34.1	34.1	34.1	34.1	34.1	34.1	34.1	34.1–42.6
BW	18.9	19.3	18.5	18.9	17.5	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.5
IND	2.5	2.6	2.4	2.5	2.3	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.3–2.6
IOD	3.5	3.6	3.6	3.6	3.5	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.5–3.7
RW	4.1	4.2	3.8	4.4	3.8	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7–3.8
RH	2.5	2.6	2.5	2.6	2.2	2.2	2.2	2.2	2.2	2.2	2.2	2.2	2.2–2.6
MW	4.5	4.4	4.1	4.7	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8–4.7
MH	2.6	2.7	2.7	3.2	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6–3.2
SL	10/11	11/11	10/11	11/11	11/11	12/11	12/11	12/11	12/11	12/11	12/11	12/11	10–12
IL	9/9	9/9	9/10	10/10	10/10	9/9	9/9	9/9	9/9	9/9	9/9	9/9	9–10

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**TABLE 1. (Continued)**

Characters	IEBR R.4991 (Holotype)	IEBR R.4992 (Paratype)	PYU.DTD 573 (Paratype)	IEBR R.5078 (Paratype)	IEBR R.5079 (Paratype)	PYU.DTD 572 (Paratype)	Min-Max
Sex	M	M	M	F	F	F	
N	6/6	6/6	6/6	6/6	6/5	6/6	5-6
IN	2	1	1	1	2	1	1-2
CIL	31	29	29	32	34	31	29-34
PM	2	2	2	2	2	2	2
GST	9 or 10	10	9	11 or 10	9 or 10	9 or 10	9-11
V	38	38	40	37	41	39	37-41
SLB	143	140	142	156	155	157	140-157
FP	3/4	3/3	2/1	0	0	0	3-7 in males
PP	5	4	5	0	0	0	4-5 in males
PAT	4/3	3/3	3/3	3/3	3/3	3/3	3-4/3
TubR	22	20	21	21	21	21	20-22
EFS	11/11	11/10	10/10	10/11	10/10	10/11	10-11
NSFIV	20	22	21	20	21	20	20-22
NSTIV	22	24	23	23	24	22	22-24

**TABLE 2.** Morphological comparisons between *Cyrtodactylus tayhoensis* sp. nov. and its 24 congeners from the *Cyrtodactylus irregularis* complex based on examination of specimens and data obtained from the literature (Smith 1921a; Heidrich et al. 2007; Orlov et al. 2007; Nazarov et al. 2008; Ngo & Bauer 2008; Rösler et al. 2008; Geissler et al. 2009; Ngo & Chan 2010; Nazarov et al. 2012; Ngo 2013; Nguyen et al. 2013; Ziegler et al. 2013; Schneider et al. 2014; Luu et al. 2017; Pauwels et al. 2018; Ngo et al. 2020; Neang et al. 2020; Ostrowski et al. 2020; Ostrowski et al. 2021; Nguyen et al. 2021; Do et al. 2021) (measurements in mm, \* = regenerated or broken tail, Max = maximum, other abbreviations defined in the text).

No.	Taxa	SVL	TaL	V	EFS	FP	PP(M)	PP(F)	LD4	LT4	Color pattern of dorsum	Enlarged subcaudals
1	<i>Cyrtodactylus tayhoensis</i> sp. nov.	82.9–94.2	max 104.3	37–41	10–11	3–7 males 0 females	4–5	0	20–22	22–24	banded	present
2	<i>C. bidoupimontis</i>	74.0–86.3	75.0–86	38–43	8–10	absent	4–6	0	15–20	18–23	banded	absent
3	<i>C. bugiamapensis</i>	58.6–76.8	65.3–83.0	36–46	6–10	absent	7–11	0–7	15–17	17–20	blotched	absent
4	<i>C. caovansungi</i>	90.4–94	120	38–44	8	6	9	0	22	23–25	banded	present
5	<i>C. cattienensis</i>	43.5–69	51–64.7	28–42	3–8	absent	6–8	0	12–16	14–19	banded	absent
6	<i>C. chungii</i>	66.6–68.5	62.8*–82.2	30–31	4–6	absent	7	6	15–18	17–20	banded	absent
7	<i>C. cryptus</i>	62.5–90.8	63.5–88.4	47–50	absent	absent	9–11	0	18–19	20–23	banded	absent
8	<i>C. cucdongensis</i>	55.8–65.9	max. 81.3	41–44	5–9	absent	5–6	4–6	13–18	15–20	banded	absent
9	<i>C. culaochamensis</i>	69.8–79.8	89.7–91.2	45–50	absent	absent	7–8	absent	18–19	20–23	banded	absent
10	<i>C. dati</i>	max 70.1	max 57.3	42–48	4–7	3–4 each	5–6	?	?	18–19	blotched	absent
11	<i>C. gialaiensis</i>	50.1–62.8	?	38–45	present	absent	9–10	0–8	14–15	15–17	Banded	absent
12	<i>C. huynhi</i>	67.2–79.8	61.5–78.6	43–46	3–5	3–8	7–9	0–8	14–17	17–21	banded	absent
13	<i>C. irregularis</i>	72–86	66.0–74	38–45	7–8	absent	5–7	0–6	15–16	18–19	blotched	absent
14	<i>C. kingsadai</i>	83–94	max 117	39–46	9–12	3–7	7–9	4–8	19–21	21–25	banded	present
15	<i>C. orlovi</i>	61–77.7	max 71.2	36–39	3–8	absent	5–6	0	15–17	16–19	banded	absent
16	<i>C. phnomchtiensis</i>	76.1–80.7	56.9–79.1	45–54	0–8	absent	4–5	1–7 pitted	18–20	20–23	banded	Absent
17	<i>C. phumyensis</i>	63.6–66.8	?	33–41	5–7	absent	5–7	6 pitted	18–19	18–21	banded	absent
18	<i>C. phuocbinhensis</i>	46–60.4	76.1	43–47	5	absent	7	0	16–21	17–19	striped/ blotched	absent

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TABLE 2. (Continued)

No.	Taxa	SVL	TaL	V	EFS	FP	PP(M)	PP(F)	LD4	LT4	Color pattern of dorsum	Enlarged subcaudals
19	<i>C. pseudoquadrivirgatus</i>	48.6–83.3	55.7–82.3	41–57	absent	absent	5–9	5–10	15–21	16–25	bande/blotched	absent
20	<i>C. raglai</i>	87.5–111.7	113.4–119	36–39	9–10	0	5	0	?	21–22	banded	present
21	<i>C. sangi</i>	49.9–56.3	47.9*	37	4	Absent	7	4 (Pitted)	?	?	banded	absent
			but just 15.1 mm original									
22	<i>C. takouensis</i>	74.7–81.1	77.7–91	39–40	3–5	0–2	3–4	0	16–17	18–20	banded	present
23	<i>C. taynguyenensis</i>	60.0–85.0	66.0–94.0	42–49	absent	absent	6	0	13–18	17–21	blotched	absent
24	<i>C. yangbayensis</i>	78.5–92.3	91.3–109.1	39–46	5–16	0–2	6–8	0	16–19	15–17	banded	Present
25	<i>C. ziegleri</i>	84.6–93.0	95.0–107.0	33–39	8–10	0–6	5–8	0–8	16–19	18–21	banded	Absent

**TABLE 3.** Morphological comparisons between *Cyrtodactylus* sp. nov. and its other congeners from Vietnam (after Smith 1921b; Ziegler et al. 2002, 2010; Nguyen et al. 2006, 2014; Hoang et al. 2007; Ngo 2008, 2011; Ngo et al. 2008, 2010; Chan & Norhayati 2010; Ngo & Grismer 2010, 2012; Luu et al. 2011; Ngo & Chan 2011; Nguyen et al. 2015, 2017; Le et al. 2016, 2021; Pham et al. 2017, 2019; Murdoch et al. 2019).

No.	Taxa	SVL	TaL	V	EFS	FP	PP(M)
1	<i>Cyrtodactylus tayhoaensis</i> sp. nov.	82.9–94.2	max 104.3	37–41	10–11	3–7 males 0 females	4–5
2	<i>C. badensis</i>	59.3–74.1	58.6–82.4	25–28	absent	absent	0
3	<i>C. bichinganae</i>	95.3–99.9	96.6*–115.6	30–31	11–13	18	10
4	<i>C. bobrovi</i>	75.2–96.4	max 95.4	40–45	absent	0	5
5	<i>C. chauquangensis</i>	90.95–99.3	97–108.3	36–38	absent	absent	6–7
6	<i>C. condorensis</i>	80	100	35–40	present	?	4–7
7	<i>C. cuephuongsensis</i>	96	79.3*	42	14	absent	0
8	<i>C. eisenmanae</i>	76.8–89.2	91–103.8	44–45	4–6	absent	0
9	<i>C. grimeri</i>	68.3–95	111.3–115.1	33–38	0–3	0	0
10	<i>C. hontreensis</i>	72.4–88.9	84.2–106.5	40–42	2–5	absent	7–8
11	<i>C. huongsonensis</i>	73.4–89.8	90.5	41–48	7–9 each	7–8 each	6
12	<i>C. intermedius</i>	61.0–85.0	80.0–100.0	40–50	6–10	?	8–10
13	<i>C. leegrimeri</i>	80.6–92	58–99	27–35	present	absent	4
14	<i>C. martini</i>	64.4–96.2	76–101.2	39–43	14–18	absent	4
15	<i>C. nigriocularis</i>	82.7–107.5	70.6–121	42–49	absent	absent	0–2
16	<i>C. ngati</i>	66.5–69.3	74.1–83.2	32–38	present	14	13
17	<i>C. otai</i>	85.2–90.6	89.7–97.6	38–43	absent	0	7–8
18	<i>C. phonghakebangensis</i>	78.5–96.3	98–110	32–42	present	present	33–42 (PP+FP)
19	<i>C. phuquocensis</i>	62.2–85.8	80.5–103.1	38–43	10–11	absent	7–9
20	<i>C. puhuensis</i>	79.24	82.59	36	?	absent	5
21	<i>C. roesleri</i>	51.1–75.3	63.4–101	34–40	7–10	present	20–28
22	<i>C. septimontium</i>	59.5–90.4	85–119	37–46	24–33	?	7–8
23	<i>C. soni</i>	88.7–103	70.6–113	41–45	8–11	6–8	6–7
24	<i>C. sonlaensis</i>	63.1–83.2	89.8–103	34–42	15–17	14–15	8
25	<i>C. taybacensis</i>	77.6–97.5	97.1–104.1	30–38	11–14	Absent	11–13

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TABLE 3. (Continued)

No.	Taxa	PP (F)	LD4	LT4	Color pattern of dorsum	Enlarged subcaudals
1	<i>Cyrtodactylus tayhoagensis</i> sp. nov.	0	20–22	22–24	banded	present
2	<i>C. badenensis</i>	0	–	18–22	banded	present
3	<i>C. bichnganae</i>	8	18–20	16–20	banded	present
4	<i>C. bobrovi</i>	0	19–21	21–22	banded	absent
5	<i>C. chauquangensis</i>	6–7	16–18	19–23	banded	present
6	<i>C. condorensis</i>	?	?	?	blotched	present
7	<i>C. cucphuongsensis</i>	?	21	24	banded	present
8	<i>C. eisenmanae</i>	0	18–20	17–18	banded	present
9	<i>C. grismeri</i>	0	16–18	16–19	banded	present
10	<i>C. honstreensis</i>	0	16	17–19	banded	present
11	<i>C. huongsonensis</i>	8	17–19	20–23	banded	present
12	<i>C. intermedius</i>	?	?	22	banded	present
13	<i>C. leegrimeri</i>	0	–	18–20	blotched	present
14	<i>C. martini</i>	0	19–23	22–24	banded	absent
15	<i>C. nigriocularis</i>	0	–	17–21	Uniformly brown	present
16	<i>C. ngati</i>	0	16–17	12–17	banded	?
17	<i>C. otai</i>	0	16–19	19–22	banded	absent
18	<i>C. phonghakebangensis</i>	0–41 (PP+FP)	15–20	18–26	banded	present
19	<i>C. phuquocensis</i>	0–8 pitted	?	15–18	banded	present
20	<i>C. puluensis</i>	?	18	23	banded	present
21	<i>C. roesleri</i>	17–22	17–19	17–21	banded	present
22	<i>C. septimontium</i>	6–8	?	17–20	Banded	?
23	<i>C. soni</i>	7–8	15–19	18–22	banded	present
24	<i>C. sonlaensis</i>	0	17–19	18–21	Banded	Present
25	<i>C. taybacensis</i>	5–15 (Pitted)	17–19	16–20	Banded	Present

uncontinuous white vertebral line extending from neck to base of tail (*versus* absent in *C. kingsadai*); from *C. bidoupimontis* Nazarov, Poyarkov, Orlov, Phung, Nguyen, Hoang & Ziegler by having a longer tail length (101.8–104.3 mm, mean ratio TL/SVL 1.20 *versus* 75–86 mm, ratio TL/SVL 1.05 in *C. bidoupimontis*), fewer scales along the midbody from mental to anterior edge of cloaca (140–157 *versus* 166–198 in *C. bidoupimontis*), the presence of femoral pores in males (3–7 *versus* absent in *C. bidoupimontis*), differences in dorsal color pattern (thinner nuchal band, divided with V-shape or triangle shape in the middle *versus* posteriorly distinctly widened nuchal band in *C. bidoupimontis*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. bidoupimontis*); from *C. bugiamapensis* Nazarov, Poyarkov, Orlov, Phung, Nguyen, Hoang & Ziegler by having a larger size (SVL 82.9–94.2 mm *versus* 58.6–76.8 mm in *C. bugiamapensis*), fewer scales along the midbody from mental to anterior edge of cloaca (140–157 *versus* 164–205 in *C. bugiamapensis*), the presence of femoral pores in males (3–7 *versus* absent in *C. bugiamapensis*), fewer precloacal pores in males (4–5 *versus* 7–8 in *C. bugiamapensis*), more lamellae under finger IV (20–22 *versus* 15–17 in *C. bugiamapensis*) and under toe IV (22–24 *versus* 17–20 in *C. bugiamapensis*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. bugiamapensis*); from *C. caovansungi* Orlov, Nguyen, Roman, Natalia & Nguyen by having fewer scales along the midbody from mental to anterior edge of cloaca (140–157 *versus* 162–187 in *C. caovansungi*), more dorsal tubercle rows (20–22 *versus* 16–18 in *C. caovansungi*), more enlarged femoral scales (10–11 *versus* 8 in *C. caovansungi*), fewer precloacal pores in males (4–5 *versus* 9 in *C. caovansungi*), and differences in dorsal color pattern (nuchal band thinner, divided with V-shape or triangle shape in the middle *versus* well developed, continuous nuchal band in *C. caovansungi*); from *C. cattienensis* Geissler, Nazarov, Orlov, Böhme, Phung, Nguyen & Ziegler by having a larger size (SVL 82.9–94.2 mm *versus* 43.5–69.0 mm in *C. cattienensis*), more enlarged femoral scales (10–11 *versus* 3–8 in *C. cattienensis*), the presence of femoral pores in males (3–7 *versus* absent in *C. cattienensis*), fewer precloacal pores in males (4–5 *versus* 6–8 in *C. cattienensis*), more lamellae under finger IV (20–22 *versus* 12–16 in *C. cattienensis*) and under toe IV (22–24 *versus* 14–19 in *C. cattienensis*), differences in dorsal color pattern (nuchal band divided with V-shape or triangle shape in the middle *versus* continuous nuchal band in *C. cattienensis*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. cattienensis*); from *C. chungii* Ostrowski, Le, Ngo, Pham, Phung, Nguyen & Ziegler by having a larger size (SVL 82.9–94.2 mm *versus* 66.6–68.5 mm in *C. chungii*), more ventral scale rows (37–41 *versus* 30–31 in *C. chungii*), more dorsal tubercle rows (20–22 *versus* 17–18 in *C. chungii*), more enlarged femoral scales (10–11 *versus* 4–6 in *C. chungii*), the presence of femoral pores in males (3–7 *versus* absent in *C. chungii*), fewer precloacal pores in males (4–5 *versus* 7 in *C. chungii*), the absence of precloacal pores in females (*versus* 6 in *C. chungii*), more lamellae under finger IV (20–22 *versus* 15–18 in *C. chungii*), and under toe IV (22–24 *versus* 17–20 in *C. chungii*), differences in dorsal color pattern (nuchal band divided with V-shape or triangle shape in the middle *versus* continuous nuchal band in *C. chungii*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. chungii*); from *C. cryptus* Heidrich, Rösler, Vu, Böhme & Ziegler by having fewer ventral scale rows (38–41 *versus* 47–50 in *C. cryptus*), the presence of enlarged femoral scales (10–11 *versus* absent in *C. cryptus*), the presence of femoral pores in males (3–7 *versus* absent in *C. cryptus*), fewer precloacal pores in males (4–5 *versus* 9–11 in *C. cryptus*), more lamellae under finger IV (20–22 *versus* 18–19 in *C. cryptus*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. cryptus*); from *C. cucdongensis* Schneider, Phung, Le, Nguyen & Ziegler by having a larger size (SVL 82.9–94.2 mm *versus* 55.8–65.9 mm in *C. cucdongensis*), higher dorsal tubercle rows (20–22 *versus* 16–19 in *C. cucdongensis*), the presence of femoral pores in males (3–7 *versus* absent in *C. cucdongensis*), the absence of precloacal pores in females (*versus* 4–6 in *C. cucdongensis*), more lamellae under finger IV (20–22 *versus* 13–18 in *C. cucdongensis*) and under toe IV (22–24 *versus* 15–20 in *C. cucdongensis*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. cucdongensis*); from *C. culaochamensis* Ngo, Grismer, Pham & Wood by having a larger size (SVL 82.9–94.2 mm *versus* 69.8–79.8 mm in *C. culaochamensis*), fewer ventral scale rows (37–41 *versus* 45–50 in *C. culaochamensis*), the presence of enlarged femoral scales (10–11 *versus* absent in *C. culaochamensis*), the presence of femoral pores in males (3–7 *versus* absent in *C. culaochamensis*), fewer precloacal pores in males (4–5 *versus* 7–8 in *C. culaochamensis*), and more lamellae under finger IV (20–22 *versus* 18–19 in *C. culaochamensis*); from *C. dati* Ngo by having a larger size (SVL 82.9–94.2 mm *versus* max 70.1 in *C. dati*), a longer tail length (101.8–104.3 mm, mean ratio TL/SVL 1.20 *versus* Max 57.3 mm, mean ratio TL/SVL: 1.06), fewer ventral scale rows (38–41 *versus* 42–48 in *C. dati*), more enlarged femoral scales (10–11 *versus* 4–7 in *C. dati*), more lamellae under toe IV (22–24 *versus* 18–19 in *C. dati*), and differences in dorsal color pattern (banded *versus* small blotched in *C. dati*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. dati*); from *C. gialaiensis* Luu, Tran, Nguyen, Le & Ziegler by having

a larger size (SVL 82.9–94.2 mm *versus* 50.1–62.8 mm in *C. gialaiensis*), fewer scales along the midbody from mental to anterior edge of cloaca (140–157 *versus* 165–178 in *C. gialaiensis*), the presence of femoral pores in males (3–7 *versus* absent in *C. gialaiensis*), fewer precloacal pores in males (4–5 *versus* 9–10 in *C. gialaiensis*), the absence of precloacal pores in adult females (*versus* 8 pitted scales in *C. gialaiensis*), more lamellae under finger IV (20–22 *versus* 14–15 in *C. gialaiensis*) and under toe IV (22–24 *versus* 15–17 in *C. gialaiensis*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. gialaiensis*); from *C. huynhi* Ngo & Bauer by having a larger size (SVL 82.9–94.2 mm *versus* 68.5–79.8 mm in *C. huynhi*), fewer ventral scale rows (37–41 *versus* 43–46 in *C. huynhi*), more dorsal tubercle rows (20–22 *versus* 16–18 in *C. huynhi*), more enlarged femoral scales (10–11 *versus* 3–5 in *C. huynhi*), fewer precloacal pores in males (4–5 *versus* 7–9 in *C. huynhi*), more lamellae under finger IV (20–22 *versus* 14–17 in *C. huynhi*) and under toe IV (22–24 *versus* 17–21 in *C. huynhi*), differences in dorsal color pattern (nuchal band divided with V-shape or triangle shape in the middle *versus* continuous nuchal band in *C. huynhi*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. huynhi*); from *C. irregularis* (Smith) by having more enlarged femoral scales (10–11 *versus* 7–8 in *C. irregularis*), the absence of precloacal pores in females (0 *versus* 0–6 in *C. irregularis*), more lamellae under finger IV (20–22 *versus* 15–16 in *C. irregularis*) and under toe IV (22–24 *versus* 18–19 in *C. irregularis*), differences in dorsal color pattern (banded *versus* blotched in *C. irregularis*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. irregularis*); from *C. orlovi* Do, Phung, Ngo, Le, Ziegler, Pham & Nguyen by having a larger size (SVL 82.9–94.2 mm *versus* 61–77.7 mm in *C. orlovi*), more enlarged femoral scales (10–11 *versus* 3–8 in *C. orlovi*), the presence of femoral pores in males (3–7 *versus* absent in *C. orlovi*), more lamellae under finger IV (20–22 *versus* 15–17 in *C. orlovi*) and under toe IV (22–24 *versus* 16–19 in *C. orlovi*), differences in dorsal color pattern (nuchal band divided with V-shape or triangle shape in the middle *versus* continuous nuchal band in *C. orlovi*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. orlovi*); from *C. phnomchiensis* Neang, Henson & Stuart by having a larger size (SVL 82.9–94.2 mm *versus* 76.1–80.7 mm in *C. phnomchiensis*), a longer tail (101.8–104.3 mm, mean ratio TL/SVL 1.20 *versus* 56.9–79.1 mm, mean ratio TL/SVL 0.88 in *C. phnomchiensis*), fewer ventral scale rows (37–41 *versus* 45–54 in *C. phnomchiensis*), more enlarged femoral scales (10–11 *versus* 0–8 in *C. phnomchiensis*), the presence of femoral pores in males (3–7 *versus* absent in *C. phnomchiensis*), the absence of precloacal pores in females (*versus* 1–7 pitted scales in *C. phnomchiensis*), differences in dorsal color pattern (nuchal band divided with V-shape or triangle shape in the middle *versus* continuous nuchal band in *C. phnomchiensis*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. phnomchiensis*); from *C. phumyensis* Ostrowski, Le, Ngo, Pham, Phung, Nguyen & Ziegler by having a larger size (SVL 82.9–94.2 mm *versus* 63.6–66.8 mm in *C. phumyensis*), more enlarged femoral scales (10–11 *versus* 5–7 in *C. phumyensis*), the presence of femoral pores in males (3–7 *versus* absent in *C. phumyensis*), the absence of precloacal pores in females (*versus* 6 pitted scales in *C. phumyensis*), more lamellae under finger IV (20–22 *versus* 18–19 in *C. phumyensis*) and under toe IV (22–24 *versus* 18–21 in *C. phumyensis*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. phumyensis*); from *C. phuocbinhensis* Nguyen, Le, Tran, Orlov, Lathrop, Macculloch, Le, Jin, Nguyen, Nguyen, Hoang, Che, Murphy & Zhang by having a larger size (SVL 82.9–94.2 mm *versus* 46.0–60.4 mm in *C. phuocbinhensis*), fewer ventral scale rows (37–41 *versus* 43–47 in *C. phuocbinhensis*), more enlarged femoral scales (10–11 *versus* 5 in *C. phuocbinhensis*), the presence of femoral pores in males (3–7 *versus* absent in *C. phuocbinhensis*), fewer precloacal pores in males (4–5 *versus* 7 in *C. phuocbinhensis*), more lamellae under toe IV (22–24 *versus* 17–19 in *C. phuocbinhensis*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. phuocbinhensis*); from *C. pseudoquadrivirgatus* Rösler, Vu, Nguyen, Ngo & Ziegler by having the presence of enlarged femoral scales (10–11 *versus* absent in *C. pseudoquadrivirgatus*), the presence of femoral pores in males (3–7 *versus* absent in *C. pseudoquadrivirgatus*), the absence of precloacal pores in females (*versus* 5–10 in *C. pseudoquadrivirgatus*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. pseudoquadrivirgatus*); from *C. raglai* Nguyen, Duong, Grismer & Poyarkov by having a shorter tail (101.8–104.3 mm, mean ratio TL/SVL 1.20 *versus* 119–135 mm, mean ratio TL/SVL 1.25 in *C. raglai*), the presence of femoral pores in males (3–7 *versus* absent in *C. raglai*), more dorsal tubercle rows (20–22 *versus* 14–15 in *C. raglai*), the presence of raised, moderately to strongly keeled body tubercles (*versus* low, weakly keeled body tubercles in *C. raglai*), and differences in dorsal color pattern (nuchal band divided with V-shape or triangle shape in the middle *versus* continuous nuchal band in *C. raglai*); from *C. sangi* Pauwels, Nazarov, Bobrov & Poyarkov by having a larger size (SVL 82.9–94.2 mm *versus* 49.9–56.3 mm in *C. sangi*), more enlarged femoral scales (10–11 *versus* 4 in *C. sangi*), the presence of femoral pores in males (3–7 *versus* absent in *C. sangi*), fewer precloacal pores in males (4–5 *versus* 7 in *C. sangi*), the



absence of precloacal pores in females (*versus* 4 pitted scales in *C. sangi*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. sangi*); from *C. takouensis* Ngo & Bauer by having a larger size (SVL 82.9–94.2 mm *versus* 74.7–81.1 mm in *C. takouensis*), more enlarged femoral scales (10–11 *versus* 3–5 in *C. takouensis*), more femoral pores in males (3–7 *versus* 0–2 in *C. takouensis*), more lamellae under finger IV (20–22 *versus* 16–17 in *C. takouensis*) and under toe IV (22–24 *versus* 18–20 in *C. takouensis*); from *C. taynguyenensis* Nguyen, Le, Tran, Orlov, Lathrop, Macculloch, Le, Jin, Nguyen, Nguyen, Hoang, Che, Murphy & Zhang by fewer ventral scale rows (38–41 *versus* 42–49 in *C. taynguyenensis*), the presence of enlarged femoral scales (10–11 *versus* absent in *C. taynguyenensis*), the presence of femoral pores in males (3–7 *versus* absent in *C. taynguyenensis*), fewer precloacal pores in males (4–5 *versus* 6 in *C. taynguyenensis*), more lamellae under finger IV (20–22 *versus* 13–18 in *C. taynguyenensis*) and under toe IV (22–24 *versus* 17–21 in *C. taynguyenensis*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. taynguyenensis*); from *C. yangbayensis* Ngo & Chan by having more femoral pores in males (3–7 *versus* 0–2 in *C. yangbayensis*), fewer precloacal pores in males (4–5 *versus* 6–8 in *C. yangbayensis*), more lamellae under finger IV (20–22 *versus* 16–19 in *C. yangbayensis*) and under toe IV (22–24 *versus* 15–27 in *C. yangbayensis*); from *C. zieglerei* Nazarov, Orlov, Nguyen & Ho by having fewer scales along the midbody from mental to anterior edge of cloaca (140–157 *versus* 173–198 in *C. zieglerei*), the absence of precloacal pores in females (*versus* 0–8 in *C. zieglerei*), more lamellae under finger IV (20–22 *versus* 16–19 in *C. zieglerei*) and under toe IV (22–24 *versus* 18–21 in *C. zieglerei*), and the presence of transversely enlarged subcaudal plates (*versus* absent in *C. zieglerei*).

## Discussion

Our discovery brings the number of bent-toed geckos reported to occur in Vietnam to 49 species (Ngo *et al.* 2022; Uetz *et al.* 2022). It further represents the 25th species of the *Cyrtodactylus irregularis* species group. In our phylogenetic analyses, the new species is placed as a sister taxon to *C. kingsadai*, the second species of the genus known from Phu Yen Province. Both species inhabit evergreen forest on granite rock. However, *C. kingsadai* has been recorded from big rocks at 50–100 m a.s.l., whereas *Cyrtodactylus tayhoaensis* **sp. nov.** has been found on smaller rocks along streams at 130–230 m a.s.l. The two species thus seem to occupy different microhabitats. Both sister taxa can also be well differentiated based on morphological and molecular distinctiveness. They are most closely related to *C. raglai* from neighboring Khanh Hoa Province (Fig. 2; Nguyen *et al.* 2021). Our field observations suggest that *Cyrtodactylus tayhoaensis* **sp. nov.** is under threat of habitat loss and degradation. Evergreen forests have been converted to agriculture land at the site and logging activities have polluted streams where the species lives. More assessments need to be undertaken to evaluate the population status and the level of threats the species is facing.

## Acknowledgments

We are grateful to the directorates of the Forest Protection Department of Phu Yen Province for their support of our work. For the fruitful cooperation within joint research projects, we cordially thank S.V. Nguyen (IEBR, Hanoi), as well as T. Pagel and C. Landsberg (Cologne Zoo). We would like to thank the local people in Son Thanh Tay Commune, Tay Hoa District for their assistance in the field and H. N. Ngo (IGR, Hanoi) for assisted laboratory work. We thank T. A. Tran (IEBR, Hanoi) for providing the map. This research is funded by the National Foundation for Science and Technology Development (NAFOSTED) under Grant Number 106.05–2020.02 and the Rufford Foundation (Grant No. 39056-1) to C.T. Pham.

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